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RAW SEQUENCE LISTING

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Application Serial Number: 10/530/880
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RAW SEQUENCE LISTING

DATE: 02/22/2006

PATENT APPLICATION: US/10/530,880

TIME: 08:26:56

Input Set : A:\2005-10-19 4600-0113PUS1.ST25.txt

Output Set: N:\CRF4\02222006\J530880.raw

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3 <110> APPLICANT: OHARA, Osamu
4     NAGASE, Takahiro
5     KIKUNO, Reiko
7 <120> TITLE OF INVENTION: NOVEL GENE AND PROTEINS ENCODED THEREBY
9 <130> FILE REFERENCE: 4600-0113PUS1
11 <140> CURRENT APPLICATION NUMBER: US 10/530,880
12 <141> CURRENT FILING DATE: 2005-04-11
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/013276
15 <151> PRIOR FILING DATE: 2003-10-16
17 <150> PRIOR APPLICATION NUMBER: JP 2002-305318
18 <151> PRIOR FILING DATE: 2002-10-21
20 <160> NUMBER OF SEQ ID NOS: 2
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 4533
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (23)..(2119)
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39 agc ccg gga atc gga gcg gga cct gcg ctg aga gcc cgg cgc tcg ccc      100
40 Ser Pro Gly Ile Gly Ala Gly Pro Ala Leu Arg Ala Arg Arg Ser Pro
41                               15                               20                               25
43 ccg ccg cgg gcc gca cgg ctg ccg cgg ctg cta gtg ctg cta gcg gcg      148
44 Pro Pro Arg Ala Ala Arg Leu Pro Arg Leu Leu Val Leu Leu Ala Ala
45                               30                               35                               40
47 gcg gcg gtg ggg ccg ggc gcg ggc ggt gcg gcg cgg ctg tac cgc gcg      196
48 Ala Ala Val Gly Pro Gly Ala Gly Gly Ala Ala Arg Leu Tyr Arg Ala
49                               45                               50                               55
51 ggc gag gac gcc gtg tgg gtg ctg gac agc ggc agc gtg cgc ggg gcc      244
52 Gly Glu Asp Ala Val Trp Val Leu Asp Ser Gly Ser Val Arg Gly Ala
53                               60                               65                               70
55 acc gcc aac agc tcg gcc gcg tgg ctc gtg cag ttc tac tcg tcg tgg      292
56 Thr Ala Asn Ser Ser Ala Ala Trp Leu Val Gln Phe Tyr Ser Ser Trp
57 75                               80                               85                               90
59 tgt ggc cac tgc atc ggc tac gcg ccc act tgg cgg gcc ctg gct ggg      340
60 Cys Gly His Cys Ile Gly Tyr Ala Pro Thr Trp Arg Ala Leu Ala Gly
61                               95                               100                               105
63 gat gtg cga gac tgg gcc agt gcc att cgc gtc gca gct ctg gac tgc      388

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65          110          115          120
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68 Met Glu Glu Lys Asn Gln Ala Val Cys His Asp Tyr Asp Ile His Phe
69          125          130          135
71 tac ccc acc ttc cgg tat ttt aaa gca ttt aca aag gag ttt aca act      484
72 Tyr Pro Thr Phe Arg Tyr Phe Lys Ala Phe Thr Lys Glu Phe Thr Thr
73          140          145          150
75 gga gaa aat ttt aaa gga cct gac cga gag ctg cga aca gtc aga cag      532
76 Gly Glu Asn Phe Lys Gly Pro Asp Arg Glu Leu Arg Thr Val Arg Gln
77 155          160          165          170
79 acg atg att gac ttc ctg cag aac cac acg gaa gga agc cgg ccc cct      580
80 Thr Met Ile Asp Phe Leu Gln Asn His Thr Glu Gly Ser Arg Pro Pro
81          175          180          185
83 gcc tgc ccg cgc cta gac ccc att cag ccc agt gat gtt ctt tcc ctt      628
84 Ala Cys Pro Arg Leu Asp Pro Ile Gln Pro Ser Asp Val Leu Ser Leu
85          190          195          200
87 ctt gac aac cgt ggc agc cat tac gtg gct att gtc ttt gaa agc aac      676
88 Leu Asp Asn Arg Gly Ser His Tyr Val Ala Ile Val Phe Glu Ser Asn
89          205          210          215
91 agc tcc tac ctt gga cgg gag gtg atc tta gac ctg atc ccg tat gaa      724
92 Ser Ser Tyr Leu Gly Arg Glu Val Ile Leu Asp Leu Ile Pro Tyr Glu
93          220          225          230
95 agc atc gtg gtg acc cga gca ctg gac ggg gac aaa gca ttt ctg gag      772
96 Ser Ile Val Val Thr Arg Ala Leu Asp Gly Asp Lys Ala Phe Leu Glu
97 235          240          245          250
99 aaa ctt ggt gtt tct tca gtc cct tcg tgt tac ctg atc tac cca aat      820
100 Lys Leu Gly Val Ser Ser Val Pro Ser Cys Tyr Leu Ile Tyr Pro Asn
101          255          260          265
103 ggg tcg cat gga ttg att aac gtc gtg aag cct ctg cgg gcc ttc ttt      868
104 Gly Ser His Gly Leu Ile Asn Val Val Lys Pro Leu Arg Ala Phe Phe
105          270          275          280
107 tcg tct tat ttg aag tca ttg ccg gat gtg agg aaa aaa tcg ctt ccc      916
108 Ser Ser Tyr Leu Lys Ser Leu Pro Asp Val Arg Lys Lys Ser Leu Pro
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111 ttg cct gaa aag cca cac aaa gaa gaa aat tca gaa atc gtg gtt tgg      964
112 Leu Pro Glu Lys Pro His Lys Glu Glu Asn Ser Glu Ile Val Val Trp
113          300          305          310
115 aga gaa ttt gac aag tcg aag ctg tac acg gtg gac ctg gag tca ggg      1012
116 Arg Glu Phe Asp Lys Ser Lys Leu Tyr Thr Val Asp Leu Glu Ser Gly
117 315          320          325          330
119 cta cac tac ctc ctg cgg gtg gag ctg gca gcc cac aag tcc ctg gcc      1060
120 Leu His Tyr Leu Leu Arg Val Glu Leu Ala Ala His Lys Ser Leu Ala
121          335          340          345
123 gga gca gag ctg aag acg ctc aag gac ttt gtg act gtc ttg gcc aag      1108
124 Gly Ala Glu Leu Lys Thr Leu Lys Asp Phe Val Thr Val Leu Ala Lys
125          350          355          360
127 ctg ttc cct gga cgg ccg cca gtc aag aag ctg ttg gag atg ctg cag      1156
128 Leu Phe Pro Gly Arg Pro Pro Val Lys Lys Leu Leu Glu Met Leu Gln

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129	365	370	375	
131	gag tgg ctg gcc agc ctt ccc ctg gac agg atc ccc tac aac gcc gtg	1204		
132	Glu Trp Leu Ala Ser Leu Pro Leu Asp Arg Ile Pro Tyr Asn Ala Val			
133	380 385 390			
135	ctt gac ctg gtc aac aac aag atg cgg att tct gga ata ttc ctt act	1252		
136	Leu Asp Leu Val Asn Asn Lys Met Arg Ile Ser Gly Ile Phe Leu Thr			
137	395 400 405 410			
139	aat cac ata aag tgg gtt gga tgt caa gga agc cga tct gag ttg agg	1300		
140	Asn His Ile Lys Trp Val Gly Cys Gln Gly Ser Arg Ser Glu Leu Arg			
141	415 420 425			
143	ggt tac ccg tgt tct ctc tgg aaa ctg ttc cac act ttg act gtt gaa	1348		
144	Gly Tyr Pro Cys Ser Leu Trp Lys Leu Phe His Thr Leu Thr Val Glu			
145	430 435 440			
147	gcc tcg acc cac cca gat gca ctg gtt ggc aca ggc ttt gaa gac gac	1396		
148	Ala Ser Thr His Pro Asp Ala Leu Val Gly Thr Gly Phe Glu Asp Asp			
149	445 450 455			
151	ccc cag gct gtg ctg cag aca atg agg agg tac gtt cac acc ttc ttt	1444		
152	Pro Gln Ala Val Leu Gln Thr Met Arg Arg Tyr Val His Thr Phe Phe			
153	460 465 470			
155	ggg tgt aag gaa tgt ggt gag cac ttt gag gaa atg gct aaa gaa tcc	1492		
156	Gly Cys Lys Glu Cys Gly Glu His Phe Glu Glu Met Ala Lys Glu Ser			
157	475 480 485 490			
159	atg gac tcg gtg aaa acc cca gac caa gcc atc ctc tgg ctg tgg aag	1540		
160	Met Asp Ser Val Lys Thr Pro Asp Gln Ala Ile Leu Trp Leu Trp Lys			
161	495 500 505			
163	aag cat aat atg gtg aac ggc cgc ctg gca ggc cat ctg agt gag gat	1588		
164	Lys His Asn Met Val Asn Gly Arg Leu Ala Gly His Leu Ser Glu Asp			
165	510 515 520			
167	ccc cgg ttt cca aag ctt cag tgg ccc act ccg gac ctc tgc cca gcc	1636		
168	Pro Arg Phe Pro Lys Leu Gln Trp Pro Thr Pro Asp Leu Cys Pro Ala			
169	525 530 535			
171	tgc cat gag gaa att aag ggc ctg gcc agc tgg gat gaa ggc cac gtg	1684		
172	Cys His Glu Glu Ile Lys Gly Leu Ala Ser Trp Asp Glu Gly His Val			
173	540 545 550			
175	ctc aca ttc ttg aag cag cac tat ggc cgc gac aac ctc tta gac acg	1732		
176	Leu Thr Phe Leu Lys Gln His Tyr Gly Arg Asp Asn Leu Leu Asp Thr			
177	555 560 565 570			
179	tat tcc gca gac cag ggg gat tcc agt gaa gga gga acc ctg gcc agg	1780		
180	Tyr Ser Ala Asp Gln Gly Asp Ser Ser Glu Gly Gly Thr Leu Ala Arg			
181	575 580 585			
183	ggt gag gaa gag gag aaa aga ctc act ccc cca gag gtg tcc cat gga	1828		
184	Gly Glu Glu Glu Glu Lys Arg Leu Thr Pro Pro Glu Val Ser His Gly			
185	590 595 600			
187	gac cga gac acc cag agc gtc cgt cca cct ggt gca ctg ggc ccc agg	1876		
188	Asp Arg Asp Thr Gln Ser Val Arg Pro Pro Gly Ala Leu Gly Pro Arg			
189	605 610 615			
191	cct gcc ctt cca gag agc ttg cat cac agc ttg gac ggg aaa ctc cag	1924		
192	Pro Ala Leu Pro Glu Ser Leu His His Ser Leu Asp Gly Lys Leu Gln			
193	620 625 630			

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200 Phe Leu Gly Val Asp Phe Ser Ser Leu Asp Met Ser Leu Cys Val Val
201 655 660 665
203 ctg tac gtg gct tca tcc ctg ttc ctc atg gtg atg tac ttc ttc ttc 2068
204 Leu Tyr Val Ala Ser Ser Leu Phe Leu Met Val Met Tyr Phe Phe Phe
205 670 675 680
207 cgg gtg agg tcc agg cgg tgg aag gtc aag cac cac cac ccg gcc gtg 2116
208 Arg Val Arg Ser Arg Arg Trp Lys Val Lys His His His Pro Ala Val
209 685 690 695
211 tga gtgcccgggt gctgccagcc acggcgggaag ctcccttgga ggcagccctg 2169
213 ccccggtgcc cctgcagctt taatatttat gatcagggat tttataaaca tgcggggcctg 2229
215 gtttcacatc ggatggcacc ttttggtctt aaagtcctgg ttttaciaaac gctcttctaa 2289
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281 tgggcgctcg tggaggtggc cccaggagtc atatggccat actcagacac acctgtgtgt 4269
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291 ttttaataaag aaatctgaca ttg 4533
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295 <211> LENGTH: 44
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of artificial sequence: Synthetic
301     oligonucleotide primer
303 <400> SEQUENCE: 2
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VERIFICATION SUMMARY

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